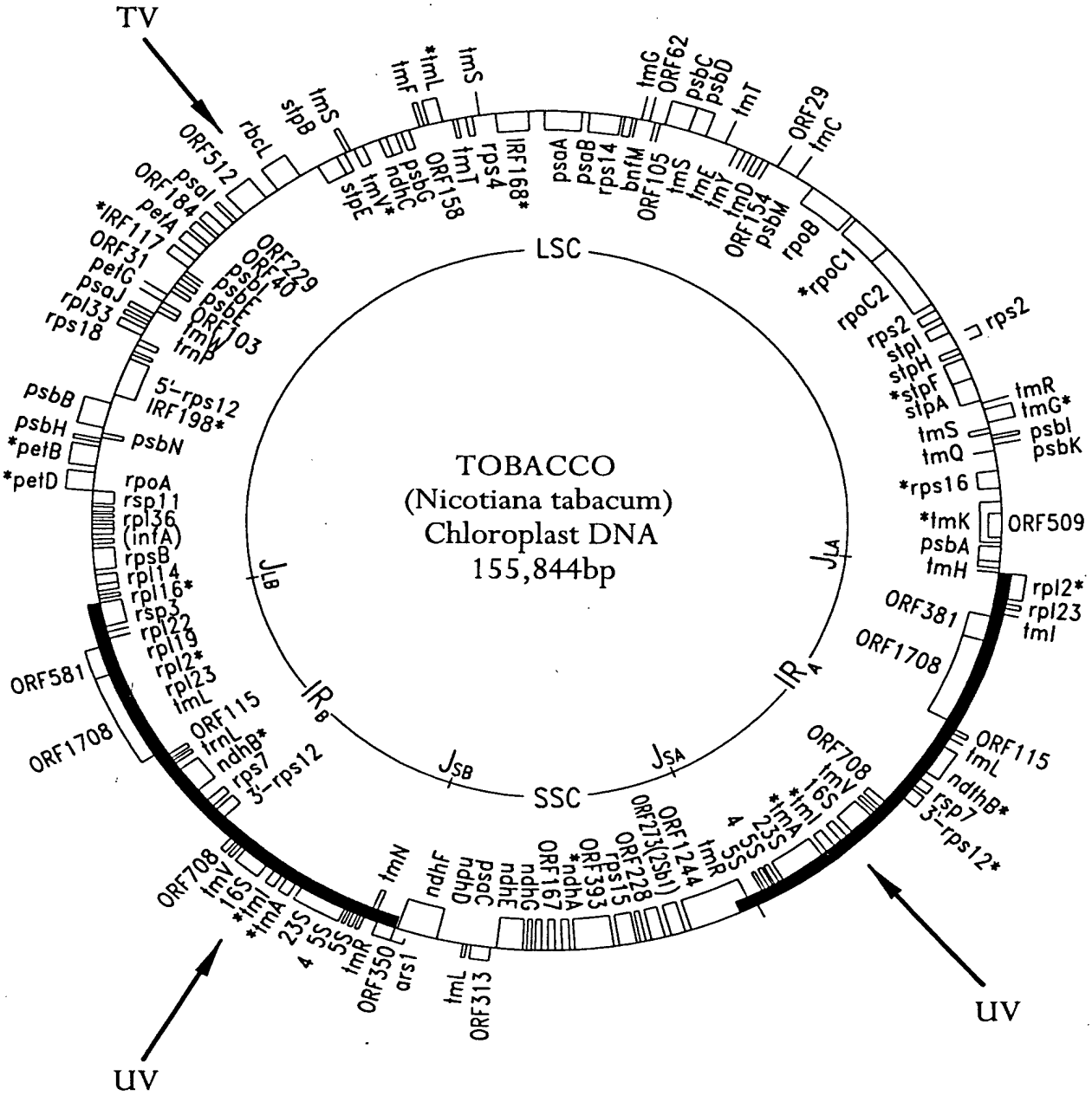


FIG. 1

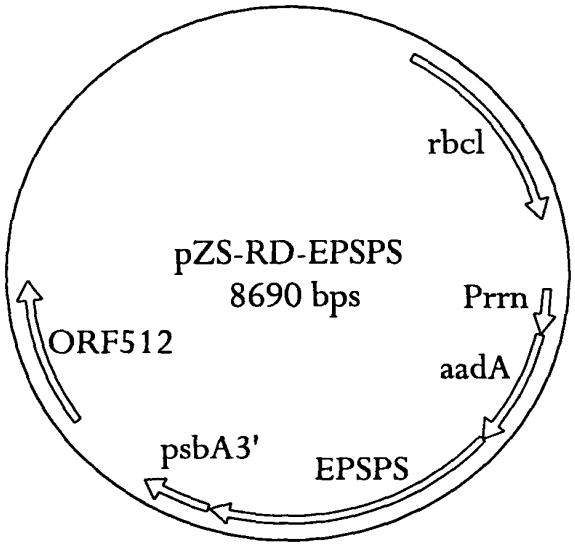


FIG. 2A

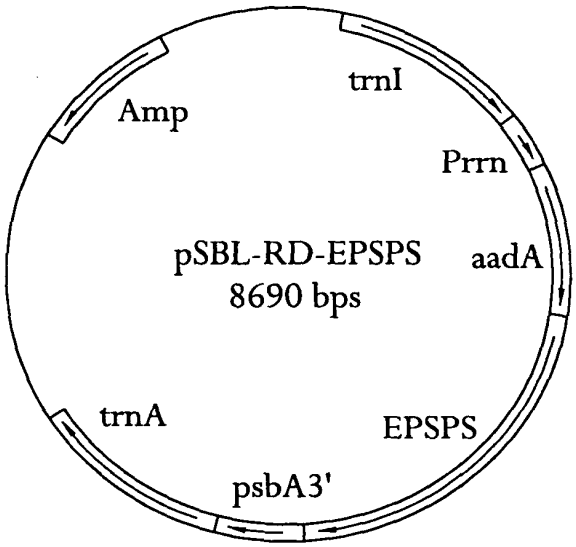


FIG. 2B

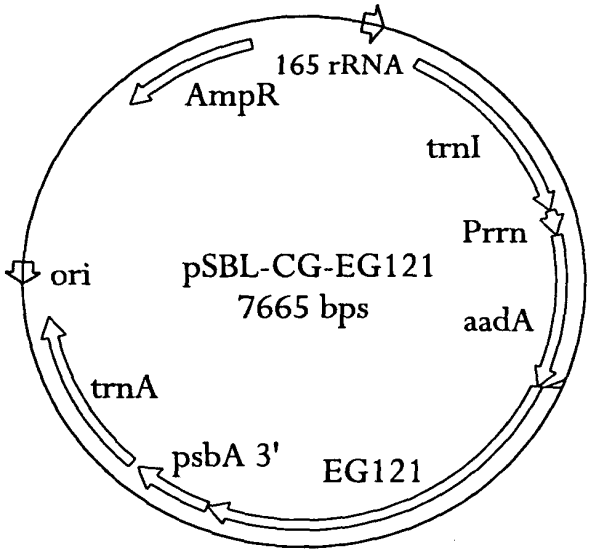


FIG. 3A

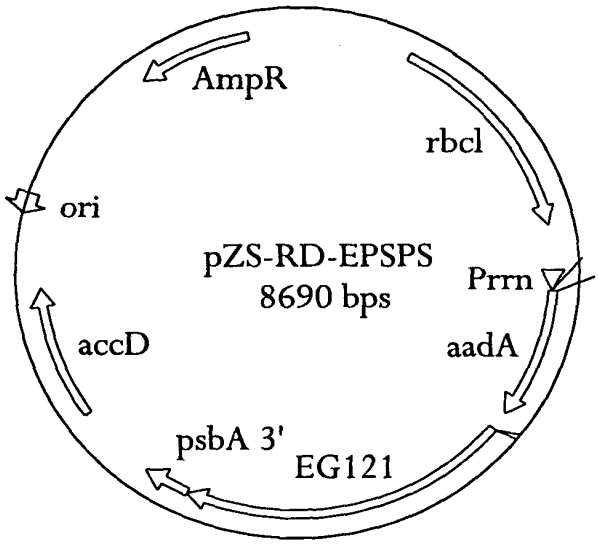
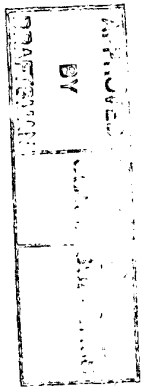


FIG. 3B

Sequence alignment of 16S-23S rDNA spacer region from several crop species

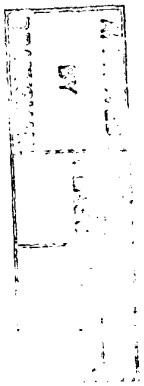
```
  ********************** ********** *   ****** ***** ******* *** ********** *****  **** * *********
S GTACACACCGCCCGTCACACTATGGGAGCTGGCCATGCC-GAAGTCGTTACC-TTAACCGCAAG-AGGGGGATGCCGAAGGCAGGGCTAGTGACTGGAGT
1 T GTACACACCGCCCGTCACACTATGGGAGCTGGCCATGCCCGAAGTCGTTACC-TTAACCGCAAGGAGGGGGATGCCGAAGGCAGGGCTAGTGACTGGAGT
M GTACACACCGCCCGTCACACTATAGGAGCTGGCCAGGTTTGAAGTCATTACCCTTAACCGTAAGGAGGGGGATGCCTAAGGCTAGGCTTGCGACTGGAGT

  ************************************************************************ *     ****** *** ****************
S GAAGTCGTAACAAGGTAGCCGTACTGGAAGGTGCGGCTGGATCACCTCCTTTTCAGGGAGAGCTAATGCTTGT------TGGGTAGTTTAGTTTGACACTGCTTCA
101 T GAAGTCGTAACAAGGTAGCCGTACTGGAAGGTGCGGCTGGATCACCTCCTTTTCAGGGAGAGCTAATGCTTGT------TGGGTATTTTGGTTTGACACTGCTTCA
M GAAGTCGTAACAAGGTAGCCGTACTGGAAGGTGCGGCTGGATCACCTCCTTTTCAGGGAGAGCTAAGTCTTATGCTTATTGGGTATTTTGGTTTGACACTGCTTCA

  * ***    *********  ** ** *******  *** ***** ***************** ***    * ************ *  ************
S CACCC-----AAAAAGAAGCGAGTTATGTCTGAGTCAAATTTGGAGATGGAAGTCTTCTTTCGTTTCTCGATGGTGAAGTAAGACTAAACTCATGAGCTTA
201 T CACCCCCAAAAAAAAGAAGGGAGCTACGTCTGAGTTAAACTTGGAGATGGAAGTCTTCTTTCCTTTCTCGACGGTGAAGTAAGACCA-GCTCATGAGCTTA
M CGCCC-----AAAAAGAAGGCAGCTACGTCTGAGCTAAACTTGGATATGGAAGTCTTCTTTCGTTT----AGGGTGAAGTAAGACCAAGCTCATGAGCTTA

  ******************** **          ******* *  ******     ******                   ******  *  ********** ** ***
S TTATCCTAGGTCGGAACAAGTT----------GATAGGAGCTACTTTTTTCA-CCCCCAT--------27bp-------ATGGGGGTGAAAAAAGGAAAGAGAGGGATGGG
301 T TTATCCTAGGTCGGAACAAGTT----------GATAGGACCCCCTTTTTTTACGTCCCCATGTTCCCCCCGTGTGGCGACATGGGGC-GAAAAAAGGAAAGAGAGGGATGGG
M TTATCCTAGGTCGGAACAAATTAGTTGATAGTGATAGGATCCCCTTTTTGACGTCCCCATGT-CCCCCCGTGTGGCGGCATGGGGATGTCAAAAGGAAAGGGATGGA----

  **** *** ********* ******** **    ******* *** ****************************************** **********
S GTTTCTCTTGCTTTTGGCATAGCGGGCCCCGGC-GGGAGGCCCGCACGACGGGCTATTAGCTCAGTGGTAGAGCGCGCCCCTGATAATTGCGTCGTTGTG
401 T GTTTCTCTCGCTTTTGGCATAGCGGGCCCCCAGTGGGAGGCTCGCACGACGGGCTATTAGCTCAGTGGTAGAGCGCGCCCCTGATAATTGCGTCGTTGTG
M GTTTTTCTCGCTTTTGGCGTAGCGGCCTCCCTTTGGGAGGC-CGCGCGACGGGCTATTAGCTCAGTGGTAGAGCGCGCCCCTGATAATT-CGTCGTTGTG
```

FIG. 4A



```
      *** * ********** ********************* ************ ***********  ************************************
    S CCTGGACTGTGAGGGC-TCTCAGCCACATGGATAGTTTAATGTGCTCATCGGCGCCTGACCCTGAGATGTGGATCATCCAAGGCACATTAGCATGGCGTA
501 T CCTGGGCTGTGAGGGCCTCTCAGCCACATGGATAGTTCAATGTGCTCATCGGCGCCTGACCCTGAGATGTGGATCATCCAAGGCACATTAGCATGGCGTA
    M CCTCGGCTGTGAGGGC-TCTCAGCCACATGGATAGTTCAATGTGCTCATCAGCGCCTGACCCGAAGATGTGGATCATCCAAGGCACATTAGCATGGCGTA

                                                                          → origin of replication (ori)
      ** ******** *** *** ***************    *  ***************************** ********** ********* *******  *****
    S CTTCTCCTGTTTGAACCGGGGTTTGAAACCAAAC----TTATCCTCAGGAGGATAGATGGGGCGATTCAGGTGAGATCCAATGTAGATCCAACTTTCTCTTCAC
601 T CTCCTCCTGTTCGAACCGGGGTTTGAAACCAAAC----TCCTCCTCAGGAGGATAGATGGGGCGATTCGGGTGAGATCCAATGTAGATCCAACTTTCGATTCAC
    M CTCCTCCTGTTTGAATCGGAGTTTGAAACCAAACAAACTTCTCCTCAGGAGGATAGATGGGGCGATTCAGGTGAGATCCCATGTAGATCGAACTTTCTATTCAC

                                                                  ori ends ↓
      ***************** *********   *****  ********************** ****************** ****** ** ***************
    S TCGTGGGATCCGGGCGATCCGGGGGGG ACCACCACGGCTCCTCTCTTCTCGAGAATTCATACATCCCTTATCAGTATATGGACAGTTATCTCTCGAGCACA
701 T TCGTGGGATCCGGGCGGTCCGGGGGG--ACCACCACGGCTCCTCTCTTCTCGAGAATCCATACATCCCTTATCAGTGTATGGACAGCTATCTCTCGAGCACA
    M TCGTGGGATCCGGGCGGTCCGGGGGGGGGCCACCGGGGCTCCTCTCTTCTCGAGAATCCATACATCCCTTATCAGTGTATGGAGAGCTATCTCTCGAGCACA

      **** **    *            **** **************** ***************************** ********************** ******
    S GGTTTAGGTTTGGCCTCAATGGAAAAAAACGGAGCACCTAACAACGTATCTTCACAGACCAAGAACTACGAGATCGCCCCTTTCATTCTGGGGTGACGGTGGGATC
801 T GGTTTAGCAATGG------GAAAATAAAATGGAGCACCTAACAACGCATCTTCACAGACCAAGAACTACGAGATCGCCCCTTTCATTCTGGGGTGACGGAGGGATC
    M GGTTGAGGTTCGTCCTCAATGGG--AAAATGGAGCACCTAACAACGCATCTTCACAGACCAAGAACTACGAGATCACCCCTTTCATTCTGGGGTGACGGAGGGATC

      ***************                  *********    ********************************** ** *********** ***  ***
    S GTACCATTCGAGCC-------260bp--------TGGGAGCAG-----GTTTGAAAAAGGATCTTAGAGTGTCTAGGGTTGTGCTAGGAGGGTCTCATAATGCCT
901 T GTACCATTCGAGCCGTTTTTTTCTTGACTCGAAATGGGAGCAG-----GTTTGAAAAAGGATCTTAGAGTGTCTAGGGTTGGGCCAGGAGGGTCTCTTAACGCCT
    M GTACCATTCGAGCC--235bp-CTTGACTCGAAATGGGAGCAGAGCAGGTTTGAAAAAGGATCTTAGAGTGTCTAGGGTTGGGCCAGGAGGGTCTCTTAACCCCT
```

FIG. 4B

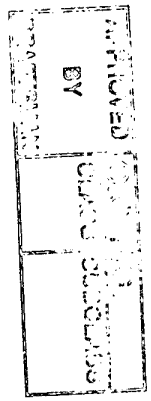


```
      ** ******* * ********************* *** ********  ***** *  ** * ** **** ********** ******************  *****
    S TCCTTTTTCTTCTCATCGGAGTTATTTCCCAAAGACTTGCCATGGTAAAGAAGA-AGGG-GGAACAAGCACACTTGGAGAGCGCAGTACAACGGATAGTTG
1001 T TCTTTTTTCTTCTCATCGGAGTTATTTCACAAAGACTTGCCAGGGTAAGGAAGA-AGGGGGGAACAAGCACACTTGGAGAGCGCAGTACAACGGAGAGTTG
    M TCTTTTTTCTGCCCATCGGAGTTATTTCCCAAGGACTTGCCGTGGTAAGGGGGAGAAGGGGGAAGAAGCACACTTGAAGAGCGCAGTACAACGGGGAGTTG

      ********************** ******************** ***************************  ***** **********************
    S TATGCTGCGTTCGGGAAGGATGAATCGCTCCCGAAAAGGAATCTATTGATTCTCTCCCAATTGGTTGGACTGTAGGTGCGATGATTTACTTCACGGGCGA
1101 T TATGCTGCGTTCGGGAAGGATGAATCGCTCCCGAAAAGGAATCTATTGATTCTCTCCCAATTGGTTGGACCGTAGGTGCGATGATTTACTTCACGGGCGA
    M TATGCTGCGTTCGGGAAGGATGGATCGCTCCCGAAAAGGAGTCTATTGATTCTCTCCCAATTGGTTGGATCGTAGGGGCGATGATTTACTTCACGGGCGA

                                        site of foreign gene insertion
      ******************** ***************** ** ************** *   *  ***** ********** ******* *********** ***
    S GGTCTCTGGTTCAAGTCCAAGATGGCCCAGCTGCGTCAAGGAAAAGAATAGAAAACTGACTTGACTCCTTCATGCATGCTCCACTCGGCTCGGGGGG-ATA
1201 T GGTCTCTGGTTCAAGTCCAGGATGGCCCAGCTGCGCCAGGGAAAAGAATAGAAGAAGCATCTGACTACTTCATGCATGCTCCACTTGGCTCGGGGGG-ATA
    M GGTCTCTGGTTCAAGTCCAGGATGGCCCAGCTGCG-CAGGGAAAAGAATAGAAGAAGCATCTGACTCTTTCATGCATACTCCACTTGGCTCGGGGGGGATA

      ********************************************************** *********** ******************************
    S TAGCTCAGTTGGTAGAGCTCCGCTCTTGCAATTGGGTCGTTGCGATTACGGGTTGGATGTCTAATTGTCTAGGCGGTAATGATAGTATCTTGTACCTGAA
1301 T TAGCTCAGTTGGTAGAGCTCCGCTCTTGCAATTGGGTCGTTGCGATTACGGGTTGGATGTCTAATTGTCCAGGCGGTAATGATAGTATCTTGTACCTGAA
    M TAGCTCAGTTGGTAGAGCTCCGCTCTTGCAATTGGGTCGTTGCGATTACGGGTTGGCTGTCTAATTGTCCAGGCGGTAATGATAGTATCTTGTACCTGAA

      ***************************** ******** ***** *************************  ** ********** ** **********
    S CCGGTGGCTCACTTTTTCTAAGTAATGGGAAAGAGGACCGAAACATGCCACTGAAAGACTCTACTGAGACAAA--GACGGGCTGTCAAGAACGTAGAGGAGG
1401 T CCGGTGGCTCACTTTTTCTAAGTAATGGGGAAGAGGACCGAAACGTGCCACTGAAAGACTCTACTGAGACAAA--GATGGGCTGTCAAGAACGTAGAGGAGG
    M CCGGTGGCTCACTTTTTCTAAGTAATGGGGAAGAGGACTGAAACATGCCACTGAAAGACTCTACTGAGACAAAAAGATGGGCTGTCAAAAAGGTAGAGGAGG
```

FIG. 4C


S TAGGATGGGCAGTTGGTCAGATCTAGTATGGATCGTACATGGACGGTAGTTGGAGTCGGTGGCTCTCCTAGGGTTTCCTCATTTGGGATC-CTGGGGAAG
1501 T TAGGATGGGCAGTTGGTCAGATCTAGTATGGATCGTACATGGACGGTAGTTGGAGTCGGCGGCTCTCCCAGGGTTCCCTCATCTGAGATCTCTGGGGAAG
M TAGGATGGGCAGTTGGTCAGATCTAGTATGGATCGTACATGGACGATAGTTGGAGTCGGCGGCTCTCCTAGGCTTCCCTCATCTGGGATCCCTGGGGAAG
S AGGATCAAGCTGGCCCTTGCGAACAGCTTGATGCACTATCTCCCTTCAACCCTTTGAGCGAAATGTGGC-----AAAAGGAAAAAGAATCCATGGACCGA
1601 T AGGATCAAGTTGGCCCTTGCGAACAGCTTGATGCACTATCTCCCTTCAACCCTTTGAGCGAAATGCGGCAAAAGAAAAGGAAGGAAAATCCATGGACCGA
M AGGATCAAGTTGGCCCTTGCGAATAGCTTGATGCACTATCTCCCTTCAACCCTTTGAGCGAAATGTGGC-----AAAAGGAAGGAAAATCCATGGACCGA
S CCCCATCGTCTCCACCCCGTAGGAACTACGAGATCACCCCAAGGAACGCCTTCGGCATCCAGGGGTCGCGGACCGACCATAGAACCCTGTTCAAAAAGCG
1701 T CCCCATCATCTCCACCCCGTAGGAACTACGAGATCACCCCAAGGAACGCCTTCGGCATCCAGGGGTCACGGACCGACCATAGAACCCTGTTCAATAAGTG
M CCCCATTGTCTCCACCCCGTAGGAACTACGAGATCACCCCAAGGAGTTCGTCCTCAATGGGGGTCTATCGGACCGACCATAG-ATCCTGTTCAATAAGTG
S GAACGCATTAGCTATCCGCTCTCAGGTTGGACAGTAAGGGTCGGAGAAGGGCAATCACTCATTCTTA-112bpGTTAGAATGGGATTCCAACTCAGCACCTTT---
1801 T GAACGCATTAGCTGTCCGCTCTCAGGTTGGGCAGTCAGGGTCGGAGAAGGGCAATGACTCATTCTTA------GTTAGAATGGGATTCCAACTCAGCACCTTTTGA
M GAACACAATAGCCGTCCGCTCTCCGGTTGGGCAGTAAGGGTCGGAGGAGGGCAATCACTCGTTCTTA-103bp-TTAGAATGGGATTCCAACTCAGCACCTTTTGT
S --TGAGATTTTGAGAAGAGTTGCTCTTTGGAGAGCACAGTACGATGAAAGTTGTGAGCTGTGTTCGGGGGGGAGTTATTGTCTATCGTTGGCCTCTATGGT
1901 T G-TGAGATTTTGAGAAGAGTTGCTCTTTGGAGAGCACAGTACGATGAAAGTTGTAAGCTGTGTTCGGGGGGGAGTTATTGTCTATCGTTGGCCTCTATGGT
M TTTGGGATTTTGAGAAGAGTTGCTCTTTGGAGAGCACAGTACGATGAAAGTTGTAAGCTGTGTTCGGGGGGGAGTTATTGCCTATCGTTGTCCTCTATGGT

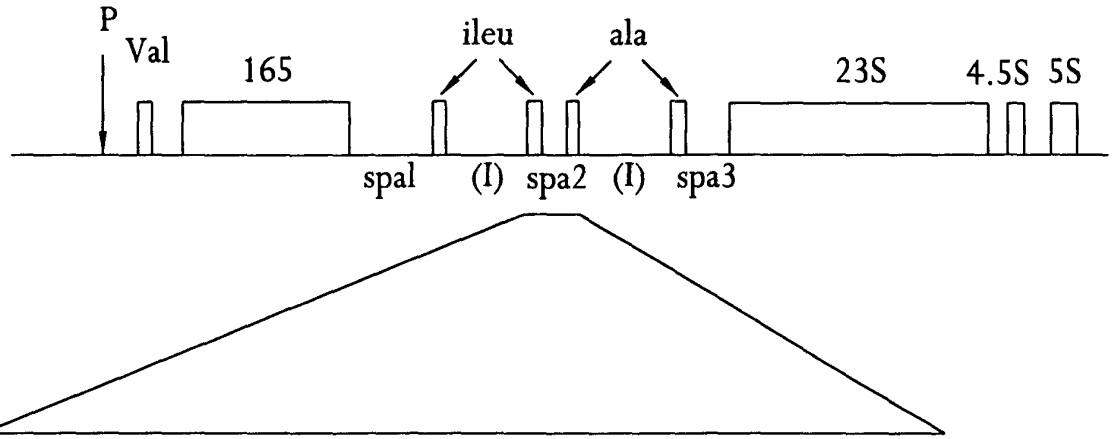
FIG. 4D



```
      **** * *******   ************************ ********************************** * ***********  *****
     S AGAATCAGTCGGGG---CCTGAGAGGCGGTGGTTTACCCTGTGGCGGATGTCAGCGGTTCGAGTCCGCTTATCTCCAACTCGTGAACTTAGTCGATACAAA
2001 T AGAATCAGTCGGGG-GACCTGAGAGGCGGTGGTTTACCCTGCGGCGGATGTCAGCGGTTCGAGTCCGCTTATCTCCAACTCGTGAACTTAGCCGATACAAA
     M AGAACCCGTCGGGGAGGCCTGAGAGGCGGTGGTTTACCCTGTGGCGGATGTCAGCGGTTCGAGTCCGCTTATCTCCAGCCCGTGAACTTAGCGGATAC---

      ***
     S GCTA
2101 T GCTT
     M ----

* indicates homology
- indicates gaps in the sequence compared to each other sequences
Nucleotide number corresponds to tobacco sequences only
S-soybean, T-tobacco, M-maize
```

FIG. 4E

GENE SEQUENCE OF rRHA CODING REGIONS IN PLASTID DNA FROM HIGHER PLANTS



SEQUENCE ALIGNMENT OF SPACER-2 (64 bp) REGION FROM SEVERAL CROP SPECIES WITH TOBACCO

```
EPIFAGUS  (90  %)     GCTGCGCTA-GGAAAAAAATATAAAAAGCATCTGATTACTTCATGCATGCT
TOBACCO (+)---      GCTGCGCCAGGGAAAAGAATAGAAGAAGCATCTGACTACTTCATGCATGCTCCA-CTTGGCTCGG
                    **** ** * * **** *  ** *      *****  ********* ***** ** ******
HELIANTHUS(96  %)     CGTGCGCCAGGGAAAAGAATAGAAGAAGCGTCTGACTCCTTCATGCATGCTCCA-CTTGGCTCGG
OENOTHERA (96  %)     GCTGCGCAAAGGAAAAGAATAGAAGAAGCATCTGACTCCTTCATGCATGCTCCA-CTTGGCTCGG
ALNUS     (95  %)     GCTGCGCCAAGTAAAAGAATAGAAGAAGCATCTGACTCCTTCATGCATGCTCCA-CTTGGCTCGG
RICE      (95  %)     GCTGCGCCAGGGAAAAGAATAGAAGAAGCATCTGACTCTTTCATGCATACTCCA-CTTGGCTCGG
MAIZE     (94  %)     GCTGCG-CAGGGAAAAGAATAGAAGAAGCATCTGACTCTTTCATGCATACTCCA-CTTGGCTCGG
SOYBEAN   (84  %)     GCTGCGTCAAGGAAAAGAATAGAAAACTGACTTGACTCCTTCATGCATGCTCCA-CTCGGCTCGG
```

FIG. 4F

```
PEA       (89  %)   GCTGCGCCAAGGAAAAGACTAAAAGACGGATTTGACTCCTTCATGCATGCTCCAACTTGGCTCGG
SPINACH   (89  %)   ACTGCGCCAAGAATAAGAATCGAAGAAGCGTCTGACTCCTTCATGCATGCTCCA-CTTGGCTCGG
                                /\
                            CGCCAGGGAA

TOBACCO   (-)---    CCGAGCCAAGTGGAGCATGCATGAAGTAGTCAGATGCTTCTTCTATTCTTTTCCCTGGCGCAGC
CUSCUTA   (96  %)   CCGAGCCAAGTGGAGCATGCATGAAGTAGTCAGATACTTCTTCGATTCTTTTCCCTGGCGCAGC
```

FIG. 4G

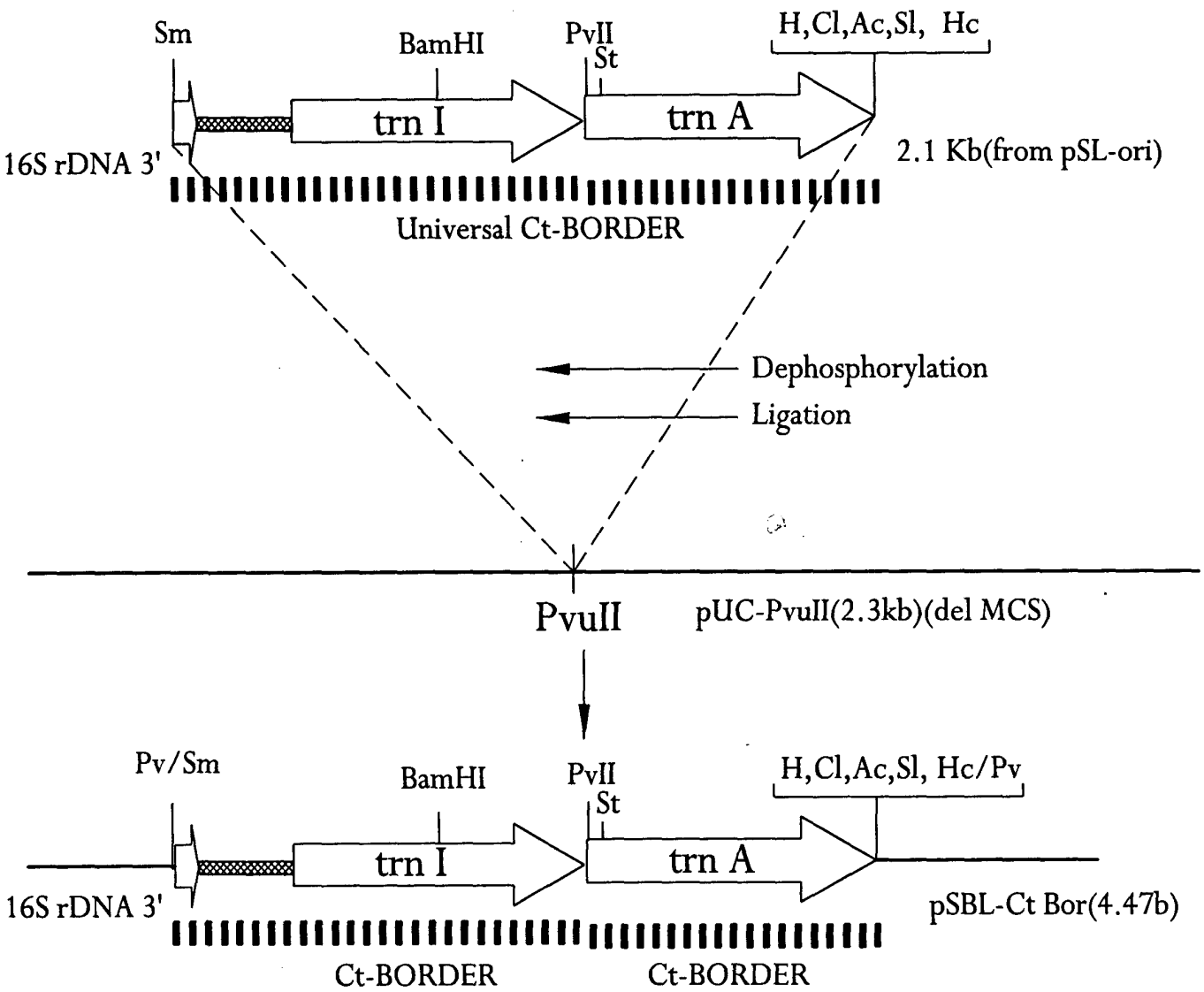


FIG. 5

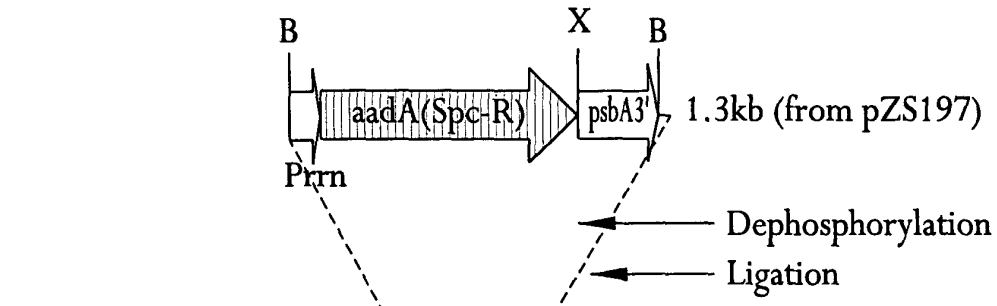


FIG. 6A

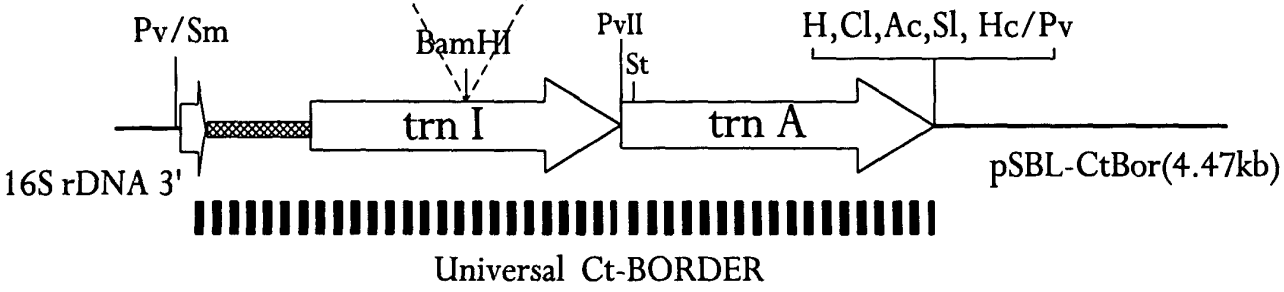


FIG. 6B

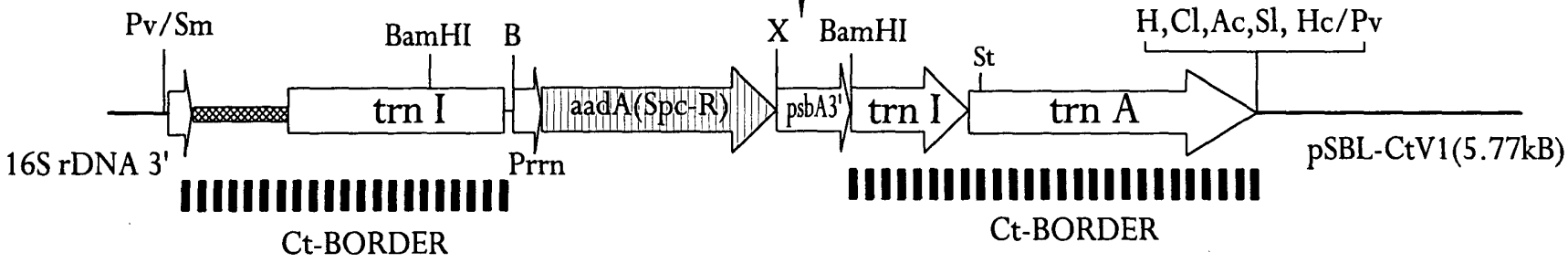


FIG. 6C

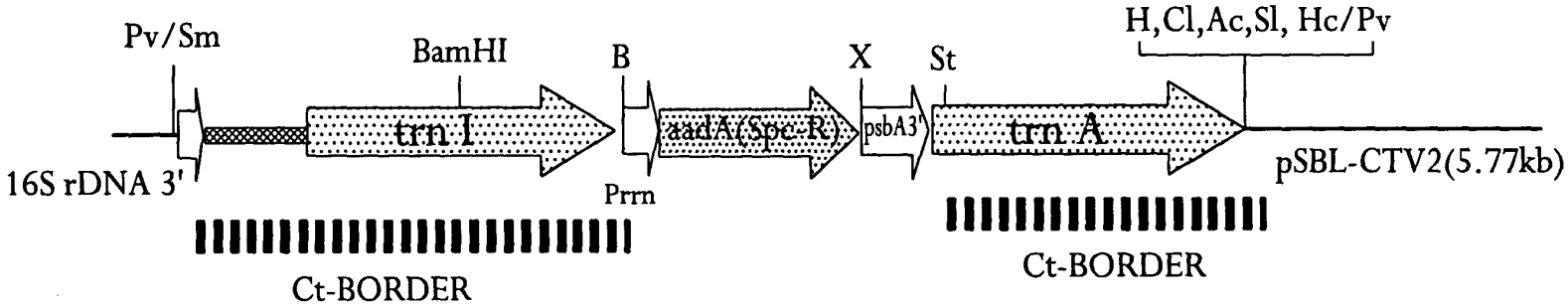


FIG. 7A

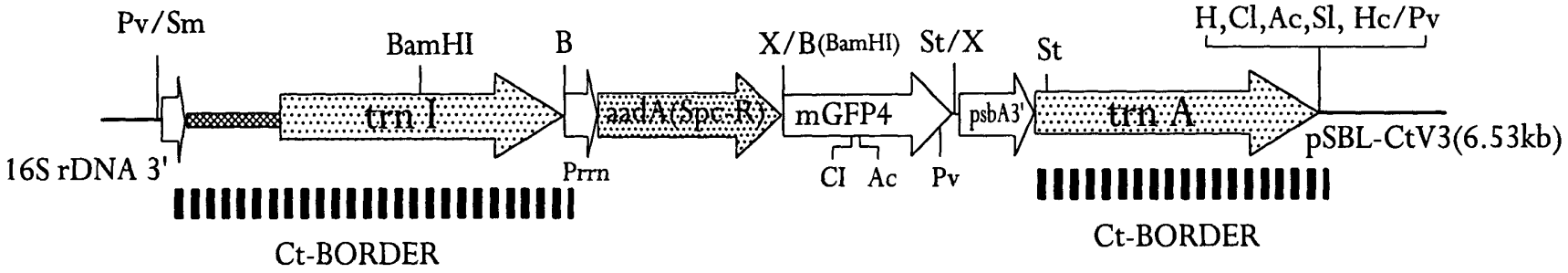


FIG. 7B

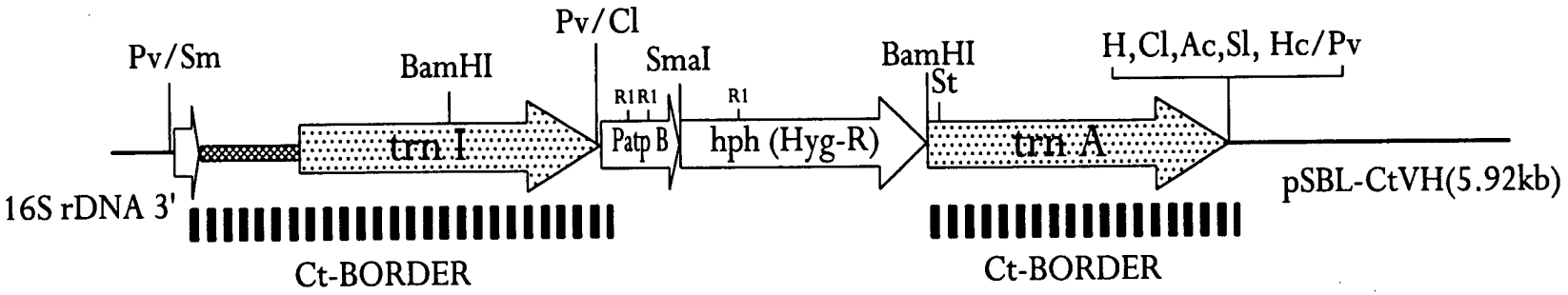


FIG. 7C

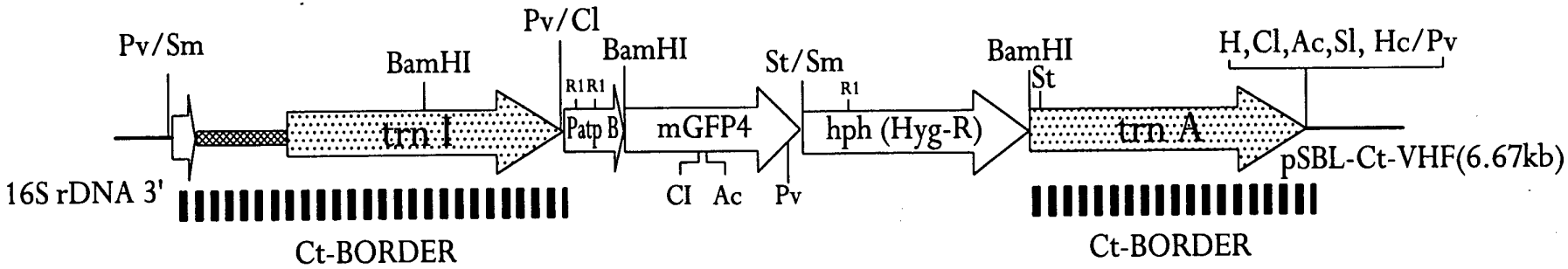


FIG. 7D

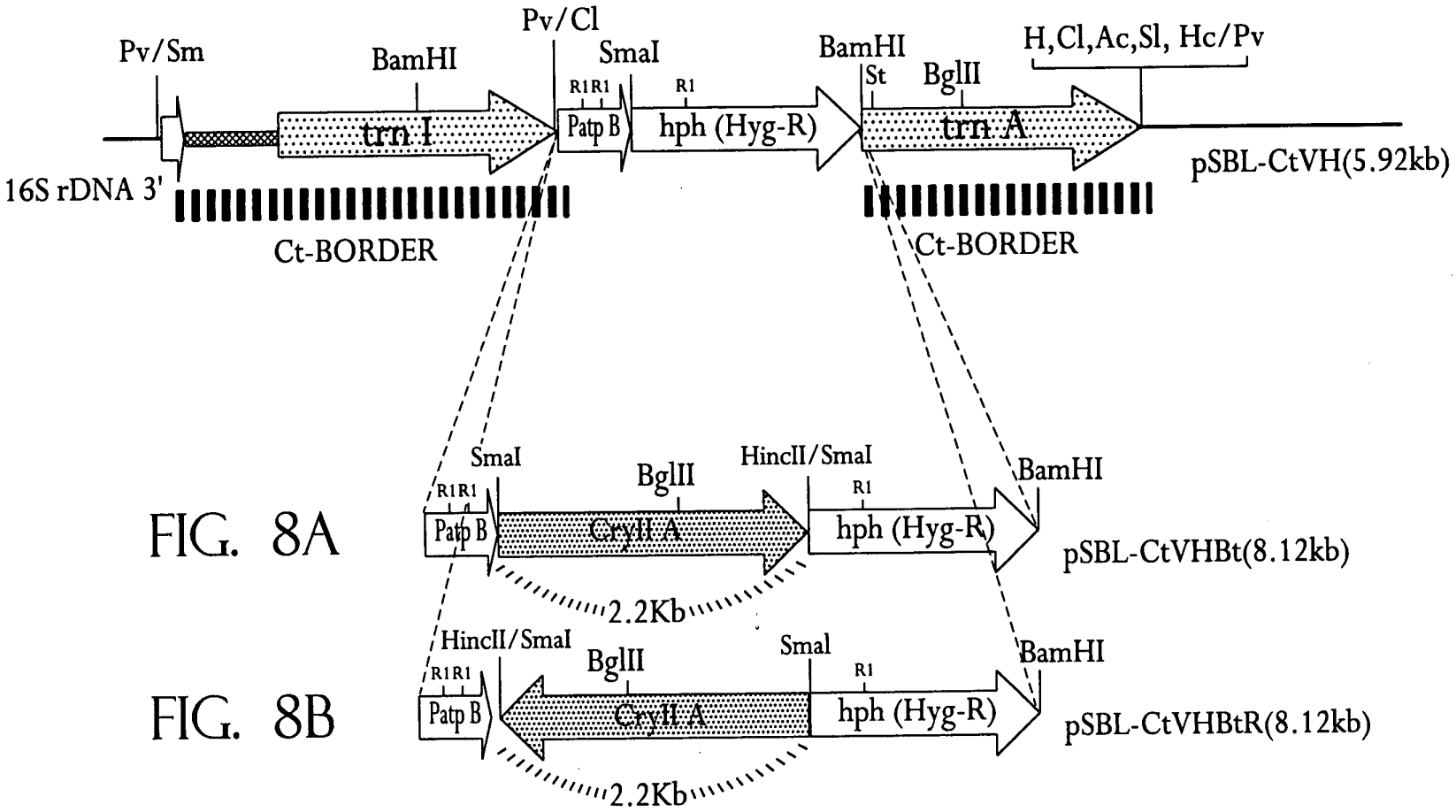


FIG. 8A

FIG. 8B

FIG. 9

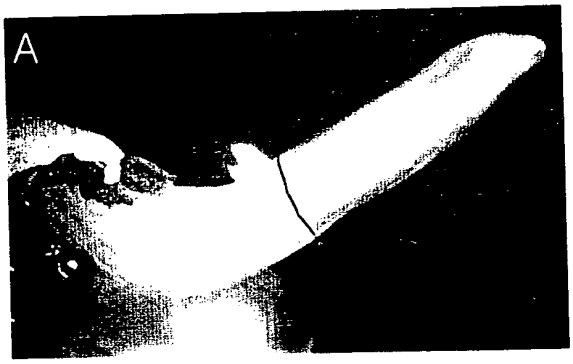


FIG. 10A

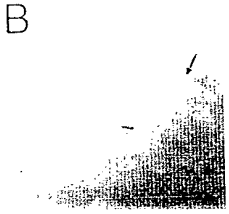


FIG. 10B

FIG. 10C

FIG. 10D

FIG. 10E

FIG. 10F

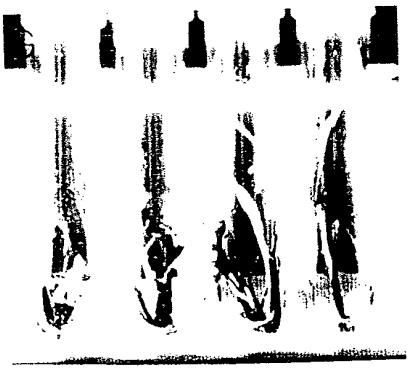


FIG. 10G

FIG. 11

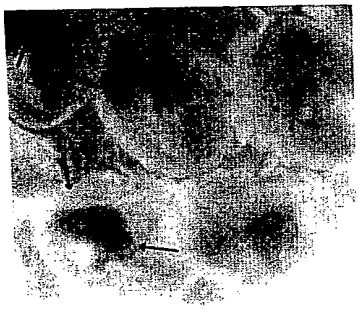


FIG. 12A

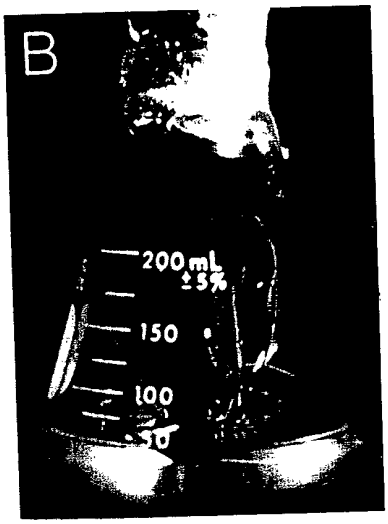


FIG. 12B

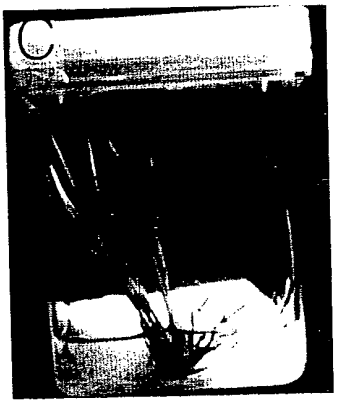


FIG. 12C

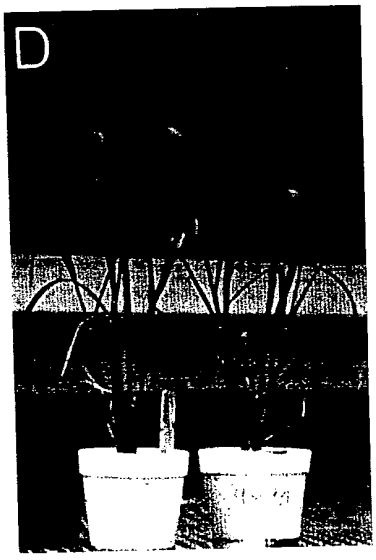


FIG. 12D

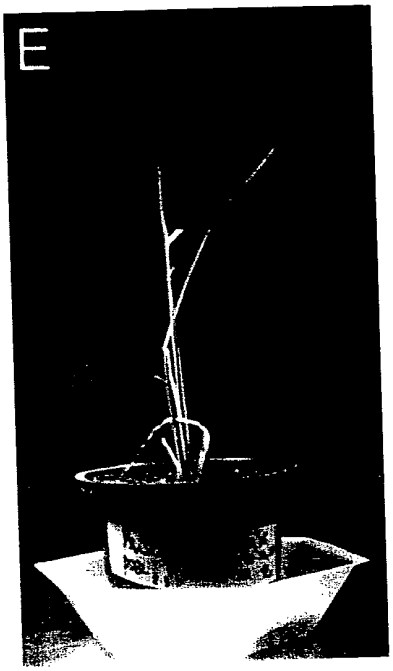


FIG. 12E

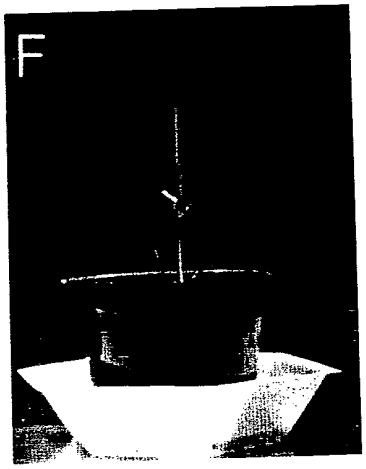


FIG. 12F

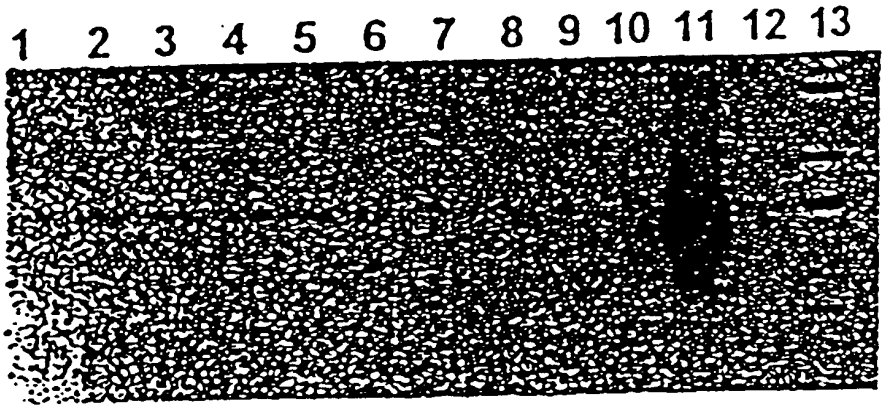


FIG. 13A

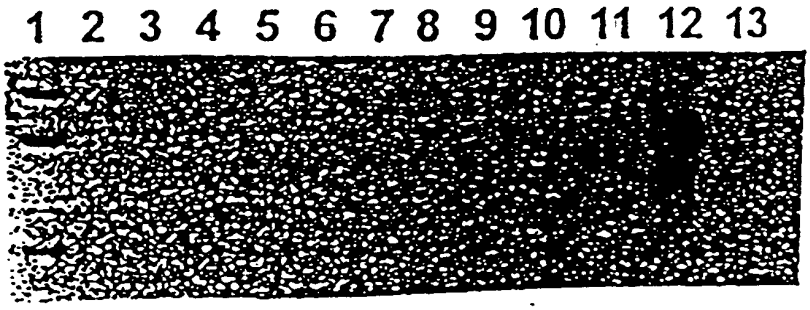


FIG. 13B

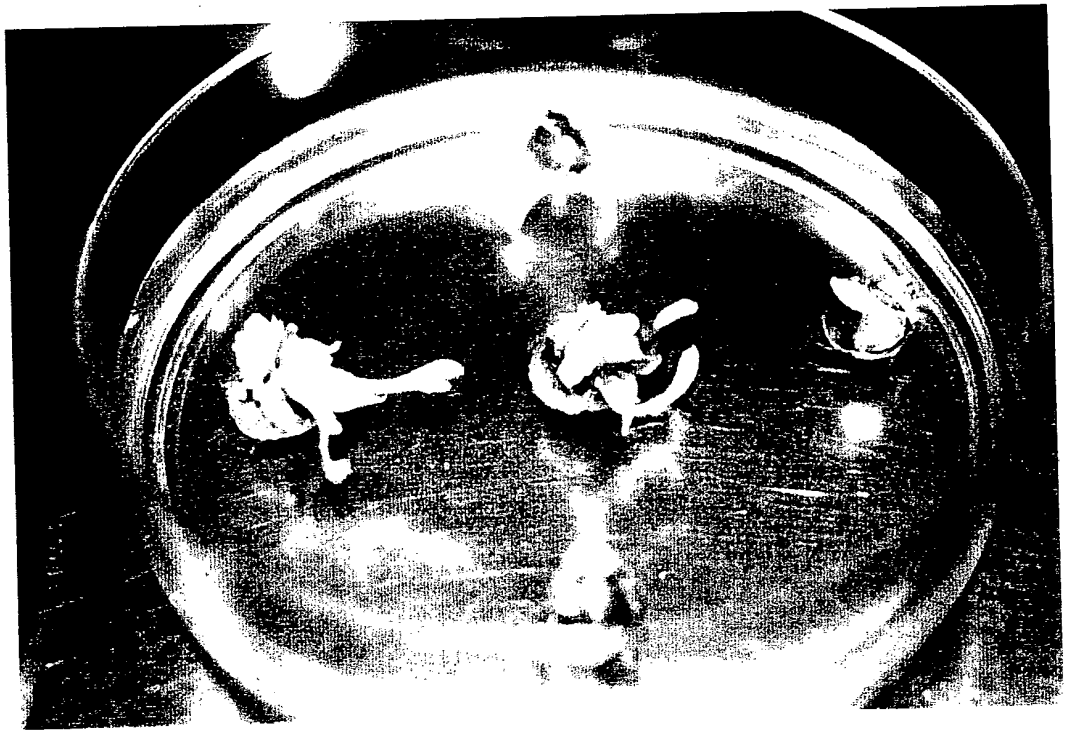


FIG. 14

FIG. 15

FIG. 16

FIG. 17

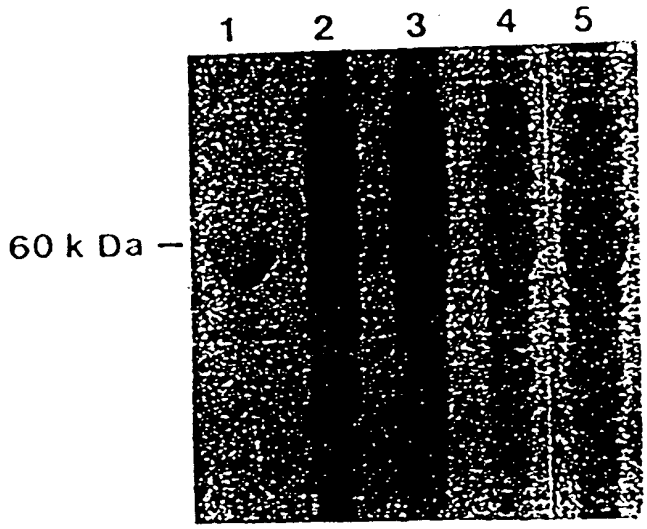


FIG. 18

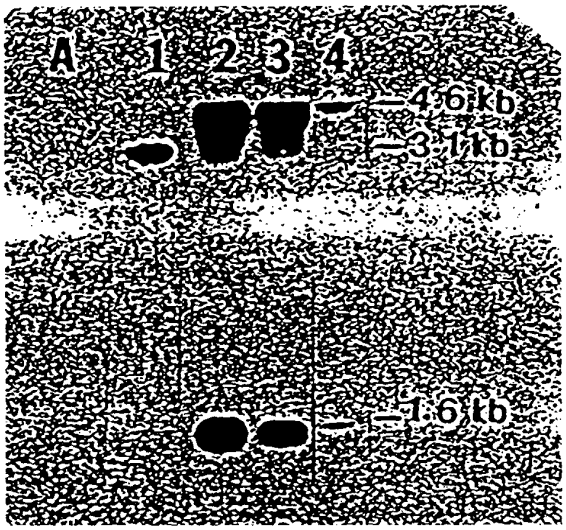


FIG. 19A

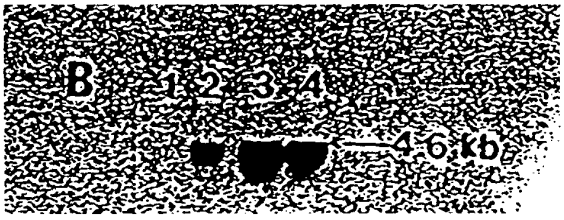


FIG. 19B

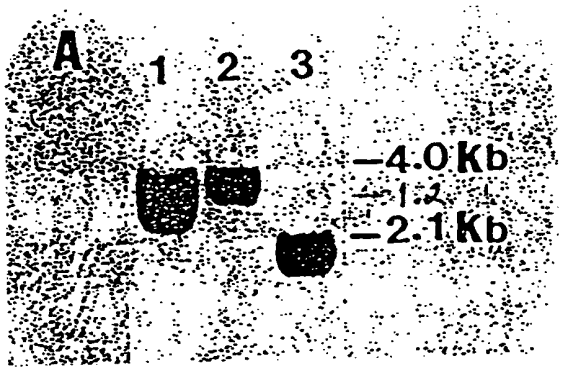


FIG. 20A

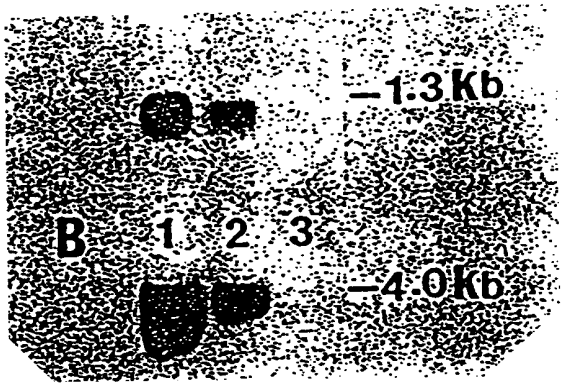


FIG. 20B

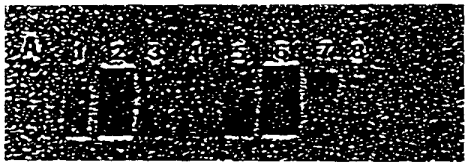


FIG. 21A

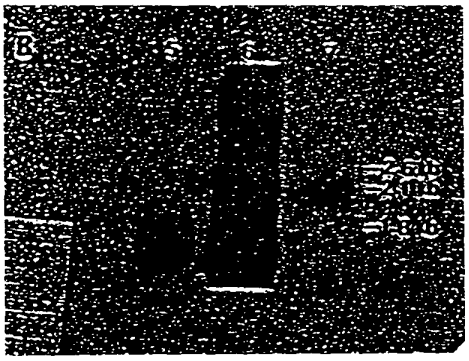


FIG. 21B

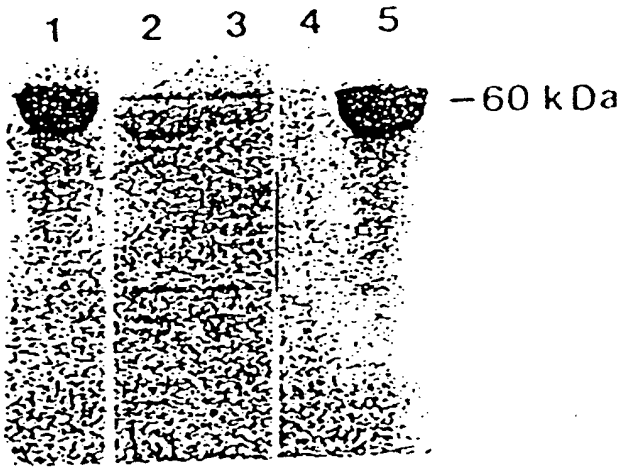


FIG. 22

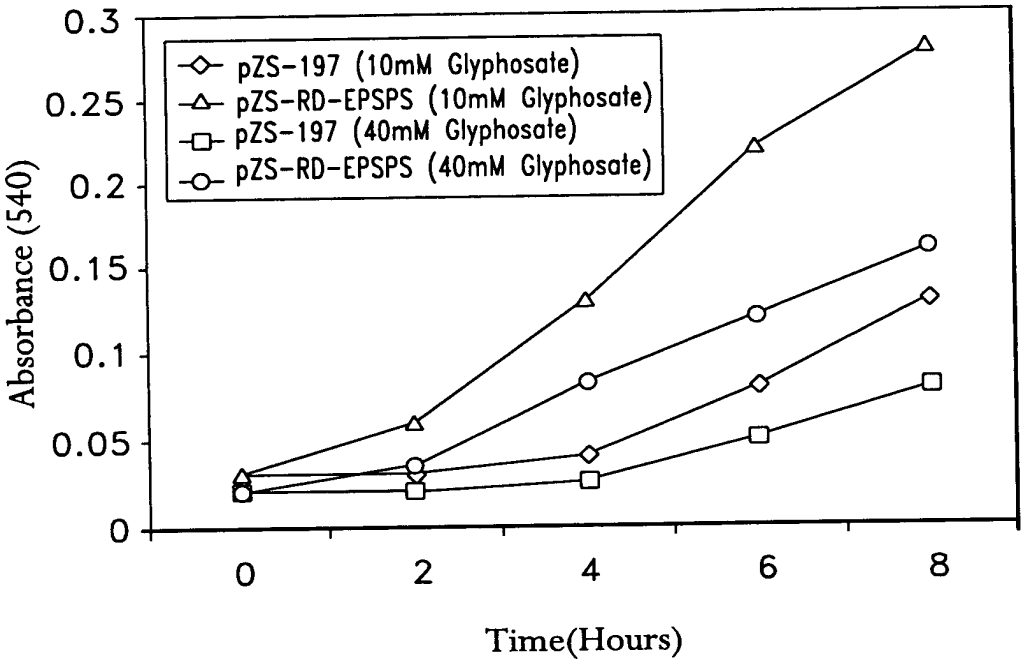


FIG. 23A

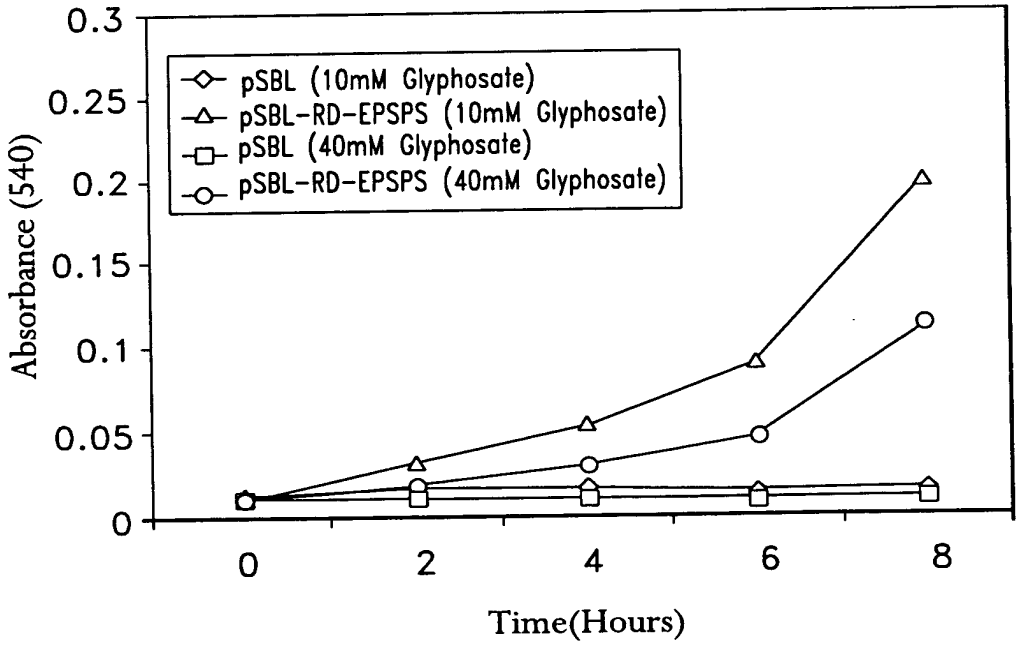


FIG. 23B

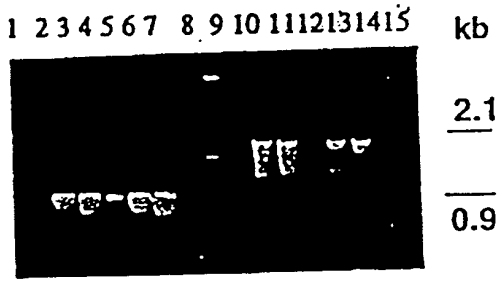


FIG. 24A

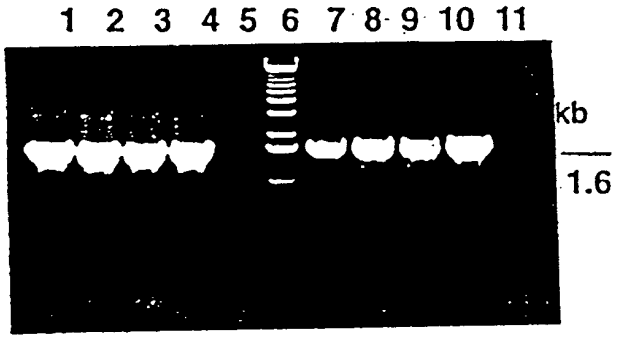


FIG. 24B

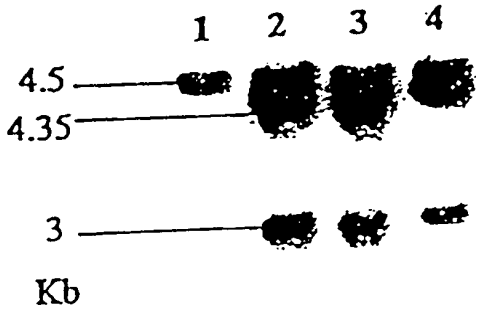


FIG. 25A

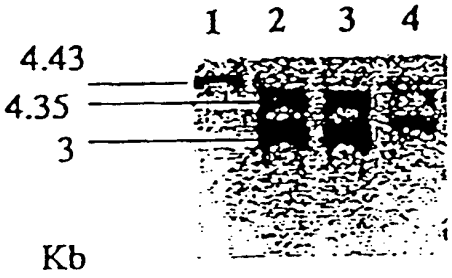


FIG. 25B

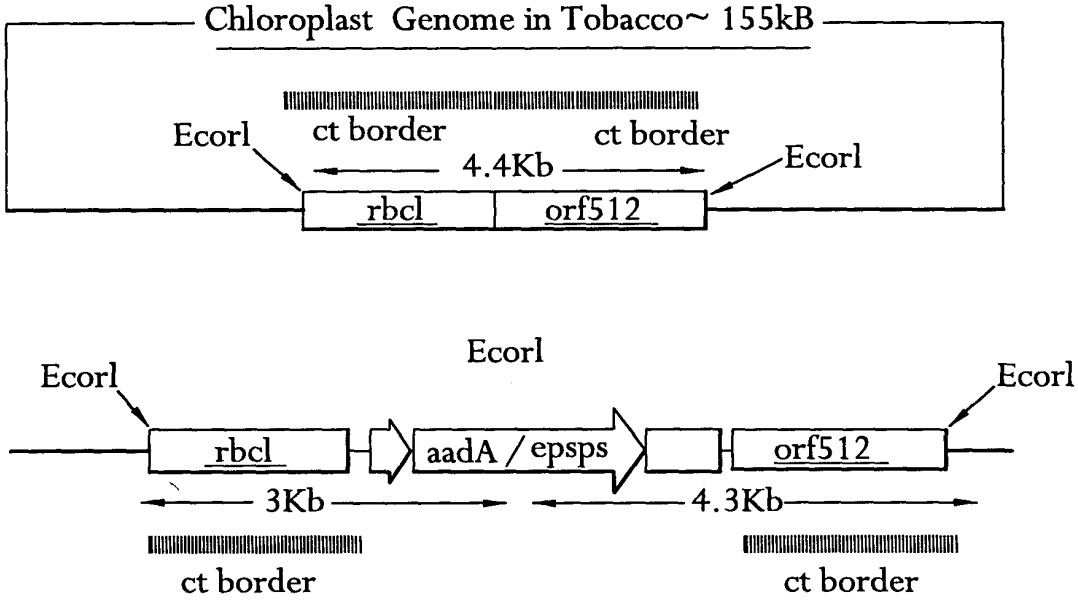

Chloroplast Genome in Tobacco~ 155kB
EcorI
ct border
ct border
4.4Kb
EcorI
rbcl
orf512
EcorI
EcorI
EcorI
rbcl
aadA / epsps
orf512
3Kb
4.3Kb
ct border
ct border
Chloroplast Genome in transgenic tobacco

FIG. 25C

A

B

FIG. 26A FIG. 26B

A

B

FIG. 27A FIG. 27B

FIG. 28A

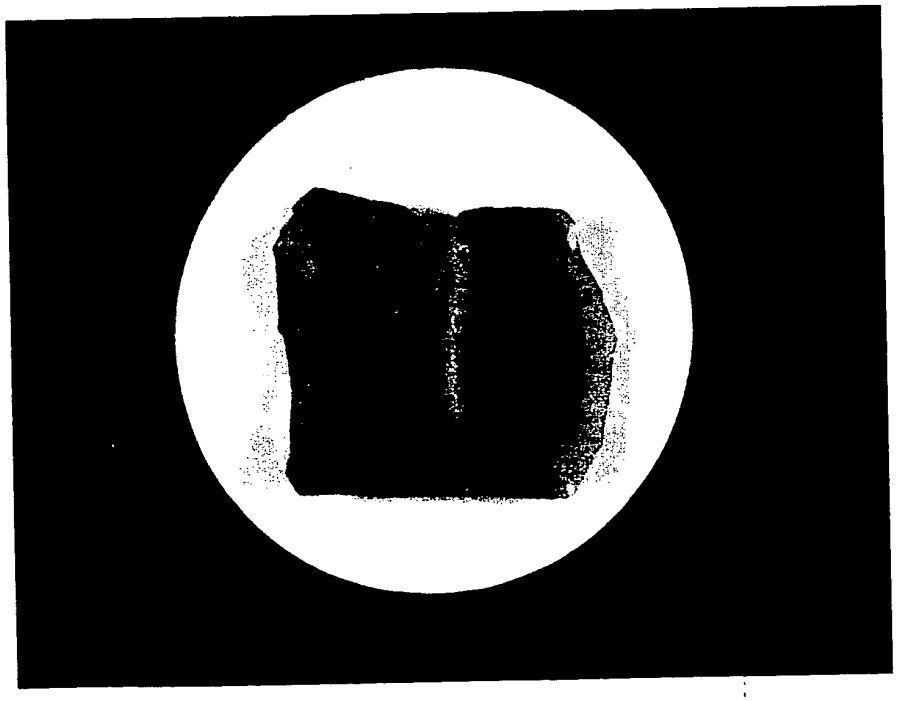


FIG. 28B

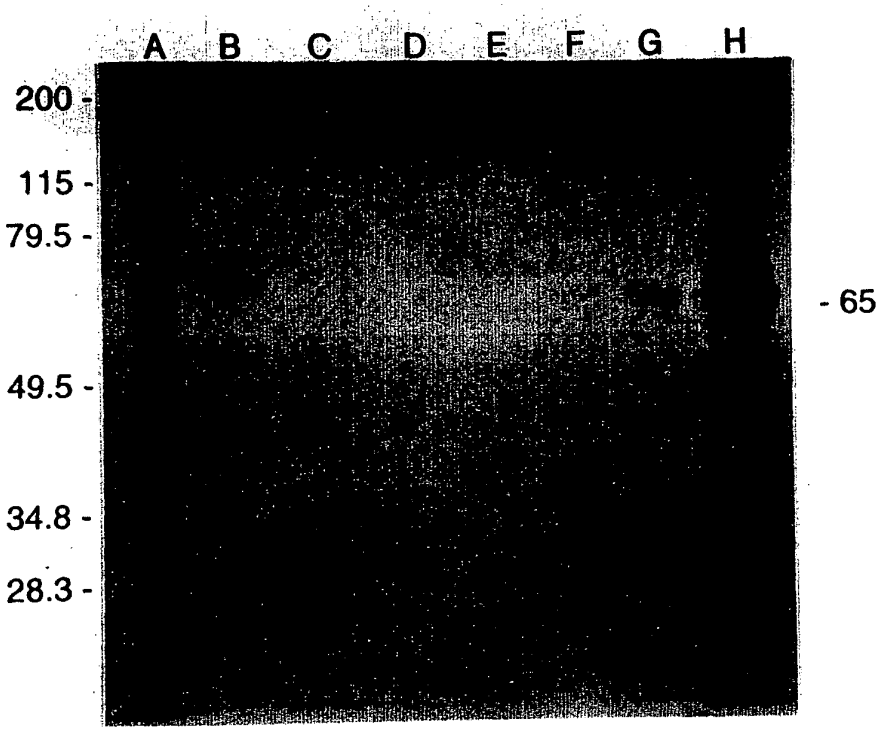


FIG. 29